

REMARKS

The amendments to the Sequence Listing submitted herein serve to conform the D and F designations for wild type and mutant lines in the Sequence Listing to those presented in the Specification.

The Sequence Listing as originally submitted inadvertently switched the header information for the D and F forms of the disclosed *Brassica* delta-12 fatty acid desaturase gene sequences. The substitute pages submitted herewith designate SEQ ID NO:1 as --Wild-type F form-- and SEQ ID NO:5 as --Wild-type D form-- in the header information.

The Sequence Listing as originally submitted was prepared by inserting the IMC 129 mutation (nucleotide 316) into SEQ ID NO:1 to create SEQ ID NO:3. As indicated above, SEQ ID NO:1 is the F form of desaturase. Because the IMC 129 mutation is in the D form, the substitute pages submitted herewith have removed the IMC 129 mutation at nucleotide 316 from SEQ ID NO:3 and inserted this mutation at the corresponding position of SEQ ID NO:7. The OTHER INFORMATION feature of SEQ ID NO:7 has been amended to read --G to A transversion mutation at nucleotide 316 of the D form--.

Support for inserting the IMC 129 mutation into SEQ ID NO:7 is found in the Specification at page 26, lines 30-32, which indicates that the IMC 129 mutation is found in the D form of the delta-12 desaturase gene. The Specification at page 60, lines 22-28 and at page 61, lines 9-12, also indicates that the IMC 129 mutation was found in the desaturase D gene.

The Sequence Listing as originally submitted was prepared by inserting the Q508 mutation into SEQ ID NO:5 to create SEQ ID NO:7. As indicated above, SEQ ID NO:5 is the D form of desaturase. Because the mutation at nucleotide 515 is in the Q508 F form, the substitute pages submitted herewith have removed the mutation at nucleotide 515 from SEQ ID NO:7 and inserted the mutation at the corresponding position of SEQ ID NO:3. The OTHER INFORMATION feature of SEQ ID NO:3 has been amended to read --T to A transversion mutation at nucleotide 515 of the F form--.

Support for inserting the Q508 mutation in SEQ ID NO:3 is found in the Specification at page 61, lines 13-20, which indicates that the mutation specific to Q508 (nucleotide 515) is found in the desaturase "F" gene.

The nucleotide sequence amendments relating to the IMC 129 and Q508 mutations are summarized in Tables 1 and 2 below.

The amino acid sequences of SEQ ID NO:2, 4, 6 and 8 have also been amended to reflect the amendments described above to the DNA sequences. The amino acid sequence amendments are also summarized in Tables 1 and 2.

The amendments to the specification at pages 14 and 25 indicate that the amino acid sequence for the wild-type D form is present in SEQ ID NO:6 and the amino acid sequence for the IMC 129 mutant D form is present in SEQ ID NO:8.

No new matter is added by these amendments.

TABLE 1.
Sequence Amendments to SEQ ID NOS:3 and 4

Nucleotide				Amino Acid		
Position	Original	As Amended	Codon as Amended	Position	Original	As Amended
316	A	G	GAG	106	Lys	Glu
515	T	A	CAC	172	Leu	His

TABLE 2.
Sequence Amendments to SEQ ID NOS:7 and 8

Nucleotide				Amino Acid		
Position	Original	As Amended	Codon as Amended	Position	Original	As Amended
316	G	A	AAG	106	Glu	Lys
515	A	T	CTC	172	His	Leu

The wild-type F and D nucleotide sequences presented in the Sequence Listing (SEQ ID NO:1 and 5, respectively) have been resequenced. Based on all the sequence data, the correct wild type F and D sequences of the Sequence Listing involves revisions as indicated in Tables 3 and 4 below.

Corresponding revisions should be made to the IMC 129 mutant D and Q508 mutant F sequences (SEQ ID NO:3 and 7, respectively). The revisions to the mutant desaturase sequences are summarized in Tables 5 and 6.

None of the corrections in Tables 3-6 have been entered into the substitute Sequence Listing enclosed herewith.

TABLE 3.
Corrections to Wild Type F Sequence

Nucleotide				Amino Acid		
Position	Submitted	Revised	Codon as Revised	Position	Submitted	Revised ¹
205	N	G	GTC	69	Xaa	Val
426	C	A	CGA	142	Arg	--
427	A	C	CGC	143	Ser	Arg
622	C	G	GCT	208	Arg	Ala
623	G	C	GCT	208	Arg	Ala
737	G	C	CGC	246	Gly	Ala
738	C	G	GCG	246	Gly	Ala
873	C	G	TTG	291	Phe	Leu
954	C	G	GCG	318	Ala	--
962	C	T	CTG	321	Pro	Leu

¹ -- = No Change in Amino Acid Sequence

TABLE 4.
Corrections to Wild Type D Sequence

Nucleotide				Amino Acid		
Position	Submitted	Revised	Codon as Revised	Position	Submitted	Revised ¹
663	C	T	CGT	221	Arg	--
736	G	R	RTC	246	Val	Ile, Val
777	G	T	CCT	259	Pro	--
784	A	R	RTT	262	Ile	Ile, Val
792	T	C	AAC	264	Asn	--
1035	T	Y	TAY	345	Tyr	--
1041	G	C	TTC	347	Leu	Phe
1042	C	G	GAT	348	His	Asp

¹ -- = No Change in Amino Acid Sequence

TABLE 5.

Corrections to Mutant Q508 F Sequence

Nucleotide				Amino Acid		
Position	Submitted	Revised	Codon as Revised	Position	Submitted	Revised
205	N	G	GTC	69	Xaa	Val
426	C	A	CGA	142	Arg	--
427	A	C	CGC	143	Ser	Arg
622	C	G	GCT	208	Arg	Ala
623	G	C	GCT	208	Arg	Ala
737	G	C	GCG	246	Gly	Ala
738	C	C	GCG	246	Gly	Ala
873	C	G	TTG	291	Phe	Leu
954	C	G	GCG	318	Ala	--
962	C	T	CTG	321	Pro	Leu

¹ -- = No Change in Amino Acid Sequence

TABLE 6.
Corrections to Mutant IMC 129 D Sequence

Nucleotide				Amino Acid		
Position	Submitted	Revised	Codon as Revised	Position	Submitted	Revised ¹
663	C	T	CGT	221	Arg	--
736	G	R	RTC	246	Val	Ile, Val
777	G	T	CCT	259	Pro	--
784	A	R	RTT	262	Ile	Ile, Val
792	T	C	AAC	264	Asn	--
1035	T	Y	TAY	345	Tyr	--
1041	G	C	TTC	347	Leu	Phe
1042	C	G	GAT	348	His	Asp

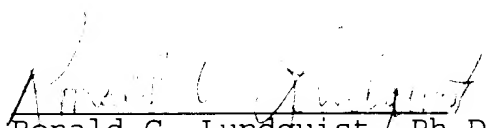
¹-- = No Change in Amino Acid Sequence

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Respectfully submitted,

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